SEQUENCE LISTING

<110>   Genetics Institute
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        Corcoran, Christopher

<120>   Aggrecanase Molecules

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<141>   2002-01-25

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65                  70                  75                  80
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Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr Ala
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Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu Tyr
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Arg Ser Pro Cys Ser Arg Ser Cys Gly Gly Gly Val Val Thr Arg Arg
65                  70                  75                  80
Arg Gln Cys Asn Asn Pro Arg Pro Ala Phe Gly Gly Arg Ala Cys Val
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Gly Ala Asp Leu Gln Ala Glu Met Cys Asn Thr Gln Ala Cys Glu Lys
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            180                 185                 190
Leu Cys Val Ser Gly Ser Cys Arg Thr Phe Gly Cys Asp Gly Arg Met
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Glu Tyr Val Thr Phe Leu Thr Val Thr Pro Asn Leu Thr Ser Val Tyr
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Ile Ala Asn His Arg Pro Leu Phe Thr His Leu Ala Val Arg Ile Gly
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Leu Gln Glu Asp Ala Asp Ile Gln Val Gly Gly Val Arg Ala Gln Leu
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65                    70                75                    80
Ala Gly Arg Glu Leu Leu Phe Pro Leu Thr Lys Gly His Ala Ser Lys
                  85                90                    95
Arg Phe His Pro Arg Ala His Ser Ser Val Pro Pro Pro Pro Gly Val
              100               105               110
His Pro Gly Thr Glu Pro Gly Leu Ser Arg Ala Leu Ser Gln Arg Met
          115               120               125
Thr Gly Ala Leu Val Trp Asp Pro Pro Arg Pro Gln Pro Gly Ser Ala
      130               135               140
Gly His Pro Arg Asn Ala His Leu Gly Leu Tyr Tyr Ser Ala Asn Glu
145               150               155               160
Gln Cys Arg Val Ala Phe Gly Pro Lys Ala Val Ala Cys Thr Phe Ala
              165               170               175
Arg Glu His Leu Val Ser Leu Pro Ala Val Ala Trp Asp Trp Leu Xaa
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Gly Pro Ser Ala Ser Pro Ser Ser Arg Pro Pro Lys Arg Ala Trp Ile
          195               200               205
Cys Ala Arg Pro Ser Pro Ala Thr Gln Thr Arg Trp Thr Lys Ala Ala
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Ala Ala Ala Ser Ser Phe Leu Ser Trp Met Gly Gln Asn Val Ala Trp
225               230               235               240
Arg Ser Gly Ala Pro Arg Val Ala Ala Ala Pro Trp Trp Ser Xaa Pro
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Pro Xaa Gln Gln Cys Met Gly Ala Gly Leu Ala Gly Val Pro Glu Val
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Leu Ala Pro Ala Pro Ala Glu Glu Val Trp Ser Pro Gly Gly Gly Ser
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6

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Asp Glu Lys Leu Pro Ala Pro Glu Pro Cys Val Gly Met Ser Cys Pro
            580             585             590
Pro Gly Trp Gly His Leu Asp Ala Thr Ser Ala Gly Glu Lys Ala Pro
            595             600             605
Ser Pro Trp Gly Ser Ile Arg Thr Gly Ala Gln Ala Ala His Val Trp
    610                 615                 620
Thr Pro Ala Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly Leu Met
625                 630                 635                 640
Glu Leu Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro Val Gln
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Glu Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg Glu Val
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Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu Ala Ala
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Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu Tyr Cys
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cacgaagaag ccgctgctcc aggacggacc acagccaccc ctgctggtgc ctccctggag   3480
tggtcccagg cccggggcct gctcttctcc ccggctcccc agcctcggcg gctcctgccc   3540
gggccccagg aaaactcagt gcagtccagt gcctgtggca ggcagcacct tgagccaaca   3600
ggaaccattg acatgcgagg cccagggcag gcagactgtg cagtggccat tgggcggccc   3660
ctcggggagg tggtgaccct ccgcgtcctt gagagttctc tcaactgcag tgcggggggac   3720
atgttgctgc tttggggccg gctcacctgg aggaagatgt gcaggaagct gttggacatg   3780
actttcagct ccaagaccaa cacgctggtg gtgaggcagc gctgcgggcg gccaggaggt   3840
ggggtgctgc tgcggtatgg gagccagctt gctcctgaaa ccttctacag agaatgtgac   3900
atgcagctct ttgggccctg gggtgaaatc gtgagcccct cgctgagtcc agccacgagt   3960
aatgcagggg gctgccggct cttcattaat gtggctccgc acgcacggat tgccatccat   4020
gccctggcca ccaacatggg cgctgggacc gagggagcca atgccagcta catcttgatc   4080
cgggacaccc acagcttgag gaccacagcg ttccatgggc agcaggtgct ctactgggag   4140
tcagagagca gccaggctga gatggagttc agcgagggct tcctgaaggc tcaggccagc   4200
ctgcggggcc agtactggac cctccaatca tgggtaccgg agatgcagga ccctcagtcc   4260
tggaagggaa aggaaggaac ctga                                          4284
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<210> 8
<211> 1427
<212> PRT
<213> homo sapiens

<400> 8

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Met His Gln Arg His Pro Trp Ala Arg Cys Pro Pro Leu Cys Val Ala
1               5                   10                  15
Gly Ile Leu Ala Cys Gly Phe Leu Leu Gly Cys Trp Gly Pro Ser His
            20                  25                  30
Phe Gln Gln Ser Cys Leu Gln Ala Leu Glu Pro Gln Ala Val Ser Ser
```

```
         35                      40                      45
Tyr Leu Ser Pro Gly Ala Pro Leu Lys Gly Arg Pro Pro Ser Pro Gly
    50                  55                  60
Phe Gln Arg Gln Arg Gln Arg Gln Arg Arg Ala Ala Gly Gly Ile Leu
65                  70                  75                  80
His Leu Glu Leu Leu Val Ala Val Gly Pro Asp Val Phe Gln Ala His
                85                  90                  95
Gln Glu Asp Thr Glu Arg Tyr Val Leu Thr Asn Leu Asn Ile Gly Ala
            100                 105                 110
Glu Leu Leu Arg Asp Pro Ser Leu Gly Ala Gln Phe Arg Val His Leu
            115                 120                 125
Val Lys Met Val Ile Leu Thr Glu Pro Glu Gly Ala Pro Asn Ile Thr
    130                 135                 140
Ala Asn Leu Thr Ser Ser Leu Leu Ser Val Cys Gly Trp Ser Gln Thr
145                 150                 155                 160
Ile Asn Pro Glu Asp Asp Thr Asp Pro Gly His Ala Asp Leu Val Leu
                165                 170                 175
Tyr Ile Thr Arg Phe Asp Leu Glu Leu Pro Asp Gly Asn Arg Gln Val
            180                 185                 190
Arg Gly Val Thr Gln Leu Gly Gly Ala Cys Ser Pro Thr Trp Ser Cys
            195                 200                 205
Leu Ile Thr Glu Asp Thr Gly Phe Asp Leu Gly Val Thr Ile Ala His
    210                 215                 220
Glu Ile Gly His Ser Phe Gly Leu Glu His Asp Gly Ala Pro Gly Ser
225                 230                 235                 240
Gly Cys Gly Pro Ser Gly His Val Met Ala Ser Asp Gly Ala Ala Pro
                245                 250                 255
Arg Ala Gly Leu Ala Trp Ser Pro Cys Ser Arg Arg Gln Leu Leu Ser
            260                 265                 270
Leu Leu Ser Ala Gly Arg Ala Arg Cys Val Trp Asp Pro Pro Arg Pro
            275                 280                 285
Gln Pro Gly Ser Ala Gly His Pro Pro Asp Ala Gln Pro Gly Leu Tyr
    290                 295                 300
Tyr Ser Ala Asn Glu Gln Cys Arg Val Ala Phe Gly Pro Lys Ala Val
305                 310                 315                 320
Ala Cys Thr Phe Ala Arg Glu His Leu Asp Met Cys Gln Ala Leu Ser
                325                 330                 335
Cys His Thr Asp Pro Leu Asp Gln Ser Ser Cys Ser Arg Leu Leu Val
            340                 345                 350
Pro Leu Leu Asp Gly Thr Glu Cys Gly Val Glu Lys Trp Cys Ser Lys
            355                 360                 365
Gly Arg Cys Arg Ser Leu Val Glu Leu Thr Pro Ile Ala Ala Val His
    370                 375                 380
Gly Arg Trp Ser Ser Trp Gly Pro Arg Ser Pro Cys Ser Arg Ser Cys
385                 390                 395                 400
Gly Gly Gly Val Val Thr Arg Arg Arg Gln Cys Asn Asn Pro Arg Pro
                405                 410                 415
Ala Phe Gly Gly Arg Ala Cys Val Gly Ala Asp Leu Gln Ala Glu Met
            420                 425                 430
Cys Asn Thr Gln Ala Cys Glu Lys Thr Gln Leu Glu Phe Met Ser Gln
            435                 440                 445
Gln Cys Ala Arg Thr Asp Gly Gln Pro Leu Arg Ser Ser Pro Gly Gly
    450                 455                 460
Ala Ser Phe Tyr His Trp Gly Ala Ala Val Pro His Ser Gln Gly Asp
465                 470                 475                 480
Ala Leu Cys Arg His Met Cys Arg Ala Ile Gly Glu Ser Phe Ile Met
                485                 490                 495
Lys Arg Gly Asp Ser Phe Leu Asp Gly Thr Arg Cys Met Pro Ser Gly
            500                 505                 510
Pro Arg Glu Asp Gly Thr Leu Ser Leu Cys Val Ser Gly Ser Cys Arg
            515                 520                 525
```

```
Thr Phe Gly Cys Asp Gly Arg Met Asp Ser Gln Gln Val Trp Asp Arg
    530               535               540
Cys Gln Val Cys Gly Gly Asp Asn Ser Thr Cys Ser Pro Arg Lys Gly
545               550               555               560
Ser Phe Thr Ala Gly Arg Ala Arg Glu Tyr Val Thr Phe Leu Thr Val
              565               570               575
Thr Pro Asn Leu Thr Ser Val Tyr Ile Ala Asn His Arg Pro Leu Phe
              580               585               590
Thr His Leu Ala Val Arg Ile Gly Gly Arg Tyr Val Val Ala Gly Lys
    595               600               605
Met Ser Ile Ser Pro Asn Thr Thr Tyr Pro Ser Leu Leu Glu Asp Gly
    610               615               620
Arg Val Glu Tyr Arg Val Ala Leu Thr Glu Asp Arg Leu Pro Arg Leu
625               630               635               640
Glu Glu Ile Arg Ile Trp Gly Pro Leu Gln Glu Asp Ala Asp Ile Gln
              645               650               655
Val Tyr Arg Arg Tyr Gly Glu Glu Tyr Gly Asn Leu Thr Arg Pro Asp
              660               665               670
Ile Thr Phe Thr Tyr Phe Gln Pro Lys Pro Arg Gln Ala Trp Val Trp
    675               680               685
Ala Ala Val Arg Gly Pro Cys Ser Val Ser Cys Gly Ala Gly Leu Arg
    690               695               700
Trp Val Asn Tyr Ser Cys Leu Asp Gln Ala Arg Lys Glu Leu Val Glu
705               710               715               720
Thr Val Gln Cys Gln Gly Ser Gln Gln Pro Pro Ala Trp Pro Glu Ala
              725               730               735
Cys Val Leu Glu Pro Cys Pro Pro Tyr Trp Ala Val Gly Asp Phe Gly
              740               745               750
Pro Cys Ser Ala Ser Cys Gly Gly Gly Leu Arg Glu Arg Pro Val Arg
    755               760               765
Cys Val Glu Ala Gln Gly Ser Leu Leu Lys Thr Leu Pro Pro Ala Arg
    770               775               780
Cys Arg Ala Gly Ala Gln Gln Pro Ala Val Ala Leu Glu Thr Cys Asn
785               790               795               800
Pro Gln Pro Cys Pro Ala Arg Trp Glu Val Ser Glu Pro Ser Ser Cys
              805               810               815
Thr Ser Ala Gly Gly Ala Gly Leu Ala Leu Glu Asn Glu Thr Cys Val
              820               825               830
Pro Gly Ala Asp Gly Leu Glu Ala Pro Val Thr Glu Gly Pro Gly Ser
    835               840               845
Val Asp Glu Lys Leu Pro Ala Pro Glu Pro Cys Val Gly Met Ser Cys
    850               855               860
Pro Pro Gly Trp Gly His Leu Asp Ala Thr Ser Ala Gly Glu Lys Ala
865               870               875               880
Pro Ser Pro Trp Gly Ser Ile Arg Thr Gly Ala Gln Ala Ala His Val
              885               890               895
Trp Thr Pro Ala Ala Gly Ser Cys Ser Val Ser Cys Gly Arg Gly Leu
              900               905               910
Met Glu Leu Arg Phe Leu Cys Met Asp Ser Ala Leu Arg Val Pro Val
    915               920               925
Gln Glu Glu Leu Cys Gly Leu Ala Ser Lys Pro Gly Ser Arg Arg Glu
    930               935               940
Val Cys Gln Ala Val Pro Cys Pro Ala Arg Trp Gln Tyr Lys Leu Ala
945               950               955               960
Ala Cys Ser Val Ser Cys Gly Arg Gly Val Val Arg Arg Ile Leu Tyr
              965               970               975
Cys Ala Arg Ala His Gly Glu Asp Asp Gly Glu Glu Ile Leu Leu Asp
    980               985               990
Thr Gln Cys Gln Gly Leu Pro Arg  Pro Glu Pro Gln Glu  Ala Cys Ser
    995               1000              1005
Leu Glu  Pro Cys Pro Pro Arg  Trp Lys Val Met Ser  Leu Gly Pro
```

10

```
          1010                      1015                        1020
Cys Ser Ala Ser Cys Gly Leu  Gly Thr Ala Arg Arg  Ser Val Ala
          1025                      1030                        1035
Cys Val Gln Leu Asp Gln Gly  Gln Asp Val Glu Val  Asp Glu Ala
          1040                      1045                        1050
Ala Cys Ala Ala Leu Val Arg  Pro Glu Ala Ser Val  Pro Cys Leu
          1055                      1060                        1065
Ile Ala Asp Cys Thr Tyr Arg  Trp His Val Gly Thr  Trp Met Glu
          1070                      1075                        1080
Cys Ser Val Ser Cys Gly Asp  Gly Ile Gln Arg Arg  Arg Asp Thr
          1085                      1090                        1095
Cys Leu Gly Pro Gln Ala Gln  Ala Pro Val Pro Ala  Asp Phe Cys
          1100                      1105                        1110
Gln His Leu Pro Lys Pro Val  Thr Val Arg Gly Cys  Trp Ala Gly
          1115                      1120                        1125
Pro Cys Val Gly Gln Gly Thr  Pro Ser Leu Val Pro  His Glu Glu
          1130                      1135                        1140
Ala Ala Ala Pro Gly Arg Thr  Thr Ala Thr Pro Ala  Gly Ala Ser
          1145                      1150                        1155
Leu Glu Trp Ser Gln Ala Arg  Gly Leu Leu Phe Ser  Pro Ala Pro
          1160                      1165                        1170
Gln Pro Arg Arg Leu Leu Pro  Gly Pro Gln Glu Asn  Ser Val Gln
          1175                      1180                        1185
Ser Ser Ala Cys Gly Arg Gln  His Leu Glu Pro Thr  Gly Thr Ile
          1190                      1195                        1200
Asp Met Arg Gly Pro Gly Gln  Ala Asp Cys Ala Val  Ala Ile Gly
          1205                      1210                        1215
Arg Pro Leu Gly Glu Val Val  Thr Leu Arg Val Leu  Glu Ser Ser
          1220                      1225                        1230
Leu Asn Cys Ser Ala Gly Asp  Met Leu Leu Leu Trp  Gly Arg Leu
          1235                      1240                        1245
Thr Trp Arg Lys Met Cys Arg  Lys Leu Leu Asp Met  Thr Phe Ser
          1250                      1255                        1260
Ser Lys Thr Asn Thr Leu Val  Val Arg Gln Arg Cys  Gly Arg Pro
          1265                      1270                        1275
Gly Gly Gly Val Leu Leu Arg  Tyr Gly Ser Gln Leu  Ala Pro Glu
          1280                      1285                        1290
Thr Phe Tyr Arg Glu Cys Asp  Met Gln Leu Phe Gly  Pro Trp Gly
          1295                      1300                        1305
Glu Ile Val Ser Pro Ser Leu  Ser Pro Ala Thr Ser  Asn Ala Gly
          1310                      1315                        1320
Gly Cys Arg Leu Phe Ile Asn  Val Ala Pro His Ala  Arg Ile Ala
          1325                      1330                        1335
Ile His Ala Leu Ala Thr Asn  Met Gly Ala Gly Thr  Glu Gly Ala
          1340                      1345                        1350
Asn Ala Ser Tyr Ile Leu Ile  Arg Asp Thr His Ser  Leu Arg Thr
          1355                      1360                        1365
Thr Ala Phe His Gly Gln Gln  Val Leu Tyr Trp Glu  Ser Glu Ser
          1370                      1375                        1380
Ser Gln Ala Glu Met Glu Phe  Ser Glu Gly Phe Leu  Lys Ala Gln
          1385                      1390                        1395
Ala Ser Leu Arg Gly Gln Tyr  Trp Thr Leu Gln Ser  Trp Val Pro
          1400                      1405                        1410
Glu Met Gln Asp Pro Gln Ser  Trp Lys Gly Lys Glu  Gly Thr
          1415                      1420                        1425
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<210> 9
<211> 11
<212> PRT
<213> Artificial
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<220>
<223>  Zinc binding signature region

<400>  9

Thr Ala Ala His Glu Leu Gly His Val Lys Phe
1                5                    10


<210>  10
<211>  28
<212>  DNA
<213>  Artificial

<220>
<223>  5' probe

<400>  10
gtgaggttgg ctgtgatatt tggagcac                                    28


<210>  11
<211>  25
<212>  DNA
<213>  Artificial

<220>
<223>  5' antisense primer

<400>  11
cgctacctga gcaggctcag cagct                                       25


<210>  12
<211>  26
<212>  DNA
<213>  Artificial

<220>
<223>  5' primer

<400>  12
cccgaagcag ttctgccccg atgttg                                      26


<210>  13
<211>  25
<212>  DNA
<213>  Artificial

<220>
<223>  5' probe

<400>  13
acccgagttg tcttcaggct ttgga                                       25


<210>  14
<211>  26
<212>  DNA
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<213>  Artificial

<220>
<223>  5' antisense primer

<400>  14
ctccacgctt catgatgaag ctctcg                                    26


<210>  15
<211>  21
<212>  DNA
<213>  Artificial

<220>
<223>  5' sense primer

<400>  15
gcggcgcctc cttctaccac t                                         21


<210>  16
<211>  25
<212>  DNA
<213>  Artificial

<220>
<223>  5' antisense primer

<400>  16
tccgtgtcgt cctcagggtt gatgg                                     25


<210>  17
<211>  25
<212>  DNA
<213>  Artificial

<220>
<223>  5' antisense primer

<400>  17
ccctcaggct ctgtcagaat gacca                                     25


<210>  18
<211>  21
<212>  DNA
<213>  Artificial

<220>
<223>  5' sense primer

<400>  18
aggggcctgg ctccgtagat g                                         21


<210>  19
<211>  23
<212>  DNA
<213>  Artificial
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<220>
<223>  5' sense primer

<400>  19
ctgggagccg gcgggaggtc tgc                                                    23


<210>  20
<211>  25
<212>  DNA
<213>  Artificial

<220>
<223>  5' probe

<400>  20
ccacaggccg tgtcttctta cttga                                                  25


<210>  21
<211>  24
<212>  DNA
<213>  Artificial

<220>
<223>  5' probe

<400>  21
ccatgggccc gggcacaata cagg                                                   24


<210>  22
<211>  26
<212>  DNA
<213>  Artificial

<220>
<223>  5' primer

<400>  22
caacatcggg gcagaactgc ttcggg                                                 26


<210>  23
<211>  24
<212>  DNA
<213>  Artificial

<220>
<223>  5' primer

<400>  23
ccatgggccc gggcacaata cagg                                                   24


<210>  24
<211>  41
<212>  DNA
<213>  Artificial
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<220>
<223> 5' primer

<400> 24
taaatcgaat tcccaccatg caccagcgtc acccctgggc a   41

<210> 25
<211> 25
<212> DNA
<213> Artificial

<220>
<223> 3' primer

<400> 25
ccacgacata gcgccctccg atcct   25

<210> 26
<211> 26
<212> DNA
<213> Artificial

<220>
<223> 5' primer

<400> 26
caacatcggg gcagaactgc ttcggg   26

<210> 27
<211> 24
<212> DNA
<213> Artificial

<220>
<223> 3' primer

<400> 27
ccatgggccc gggcacaata cagg   24

<210> 28
<211> 21
<212> DNA
<213> Artificial

<220>
<223> 5' primer

<400> 28
aggggcctgg ctccgtagat g   21

<210> 29
<211> 41
<212> DNA
<213> Artificial

<220>

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<223>   3' primer

<400>   29
atagtttagc ggccgctcag gttccttcct ttcccttcca g                    41


<210>   30
<211>   15
<212>   DNA
<213>   Artificial

<220>
<223>   5' insert

<400>   30
catgggcagc tcgag                                                 15


<210>   31
<211>   34
<212>   DNA
<213>   Artificial

<220>
<223>   5' intermediate of pMT21

<400>   31
ctgcaggcga gcctgaattc ctcgagccat catg                            34


<210>   32
<211>   68
<212>   DNA
<213>   Artificial

<220>
<223>   5' adapter

<400>   32
cgaggttaaa aaacgtctag gcccccccgaa ccacggggac gtggtttttcc tttgaaaaac   60
acgattgc                                                         68
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